

Patent 9,436,850

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Inventors: Hillman et al.

Title: NOVEL HUMAN MEMBRANE PROTEIN

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#4

9	18	27	36	45	54
5' GGC TTC TGG GAG CNA CCG CTC CGC TCG TCT CGT TGG TTC CGG AGG TCG CTG CGG					
63	72	81	90	99	108
CGG TGG GAA ATG CTG GCG CGC GCG GCG GCG CAC TGG GGC CCT TTT GCT GAG					
M L A R A A R G H W G P F A E					
117	126	135	144	153	162
GGG CTC TCT ACT GGC TTC TGG CCG CGC TCC GGC CGC GCC TCC TCT GGA TTG CCC					
G L S T G F W P R S G R A S S G L P					
171	180	189	198	207	216
CGA AAC ACC GTG GTA CTG TTC GTG CCG CAG CAG GAG GCC TGG GTG GTG GAG CGA					
R N T V V L F V P Q Q E A W V V E R					
225	234	243	252	261	270
ATG GGC CGA TTC CAC CGG ATC CTG GAG CCT GGT TTG AAC ATC CTC ATC CCT GTG					
M G R F H R I L E P G L N I L I P V					
279	288	297	306	315	324
TTA GAC CGG ATC CGA TAT GTG CAG AGT CTC AAG GAA ATT GTC ATC AAC GTG CCT					
L D R I R Y V Q S L K E I V I N V P					
333	342	351	360	369	378
GAG CAG TCG GCT GTG ACT CTC GAC AAT GTA ACT CTG CAA ATC GAT GGA GTC CTT					
E Q S A V T L D N V T L Q I D G V L					

FIGURE 1A

387	TAC CTG CGC ATC ATG GAC CCT TAC AAG GCA AGC TAC GGT GTG GAG GAC CCT GAG	405	414	423	432
	Y L R I M D P Y K A S Y G V E D P E				
441	TAT GCC GTC ACC CAG CTA GCT CAA ACA ACC ATG AGA TCA GAG CTC GGC AAA CTC	459	468	477	486
	Y A V T Q L A Q T T M R S E L G K L				
495	TCT NTG GAC AAA GTC TTC CGG GAA CGG GAG TCC CTG AAT GCC AGC ATT GTG GAT	513	522	531	540
	S X D K V F R E R E S L N A S I V D				
549	GCC ATC AAC CAA GCT GCT GAC TGC TGG GGT ATC CGC TGC CTN CGT TAT GAG ATC	567	576	585	594
	A I N Q A A D C W G I R C L R Y E I				
603	AAG GAT ATC CAT GTG CCA CCC CGG GTG AAA GAG TCT ATG CAG ATG CAG GTG GAG	621	630	639	648
	K D I H V P P R V K E S M Q M Q V E				
657	GCA GAG CGG CGG AAA CGG GCC ACA GTT CTA GAG TCT GAG GGG ACC CGA GAG TCG	675	684	693	702
	A E R R K R A T V L E S E G T R E S				
711	GCC ATC AAT GTG GCA GAA GGG AAG AAA CAG GCC CAG ATC CTG GCC TCC GAA GCA	729	738	747	756
	A I N V A E G K K Q A Q I L A S E A				

FIGURE 1B

765	774	783	792	801	810
GAA AAG GCT GAA CAG ATA AAT CAG GCA GGA GAG GCC AGT GCA GTT CTG GCG					
E K A E Q I N Q A A G E A S A V L A					
819	828	837	846	855	864
AAG GCC AAG GCT AAA GCT GAA GCT ATT CGA ATC CTG GCT GCA GCT CTG ACA CAA					
K A K A A K A E A I R I L A A L T Q					
873	882	891	900	909	918
CAT AAT GGA GAT GCA GCA GCT TCA CTG ACT GTG GCC GAG CAG TAT GTC AGC GCG					
H N G D A A A S L T V A E Q Y V S A					
927	936	945	954	963	972
TTC TCC AAA CTG GCC AAG GAC TCC AAC ACT ATC CTA CTG CCC TCC AAC CCT GGC					
F S K L A K D S N T I L L P S N P G					
981	990	999	1008	1017	1026
GAT GTC ACC AGC ATG GTG GCT CAG GCC ATG GGT GTA TAT GGA GCC CTC ACC AAA					
D V T S M V A Q A M G V Y G A L T K					
1035	1044	1053	1062	1071	1080
GCC CCA GTG CCA GGG ACT CCA GAC TCA CTC TCC AGT GGG AGC AGC AGA GAT GTC					
A P V P G T P D S L S S G S R D V					
1089	1098	1107	1116	1125	1134
CAG GGT ACA GAT GCA AGT NTT GAT GAG GAA CTT GAT CGA GTC AAG ATG AGT TAG					
Q G T D A S X D E E L D R V K M S *					

FIGURE 1C

5'-GTGGGAGG-3'

1143 TGG AGC TGG GCT TNG CCA GGG AGT CTG GGG ACA AGG AAG CAG ATT TTC CTG ATT 1188

3'

FIGURE 1D

1	MLARAARGHWG	----	PFAEGLSTGFWPRS	----	GR	789094
1	MAEKRRHTRDSE	----	A--QRLPDSFKDSP	----	SK	GI 31069
1	MNLKTCSLSTH	----	SFLQKKNEKHDGNP	----	EH	GI 1065452
1	MEYGMPEGSYDSVFTYA	----	PYNDLDKMGYMGPARQGMMMLGNK	----	GI	1353669
1	MQGA	----	----	----	----	79701
1	M	----	----	----	W	GI 1591514
28	ASS	----	GLPR	----	NTVVL	789094
26	----	----	GLGPCGWIILVAFSFLFTVITF	----	GI	31069
28	YDT	----	GLGFCGWFMLMGLSWIMVISTF	----	GI	1065452
41	YGNFTYTRDYGVNMEDDIKPLSAIELLIFCVSFLFVMTM	----	VAGLVFLAVLVIF	----	GI	1353669
5	----	----	WLI	----	GI	79701
9	F	----	WLI	----	GI	1591514
41	----	----	VPOQEA	----	ILLEPG	789094
47	PISIMM-CIKI	----	IFRLGRILQGGA	----	FFIL	GI 31069
52	PVSIYF-CMKV	----	IFRLGRILQGGA	----	FFIL	GI 1065452
81	PLSLLF-ALKFISTSEKLVVRLR	----	GRVSR	----	TVSGQL	GI 1353669
18	AIIVVAKSVALLIPQAEAVIE	----	RLGRVSR	----	TVSGQL	GI 79701
24	----	----	AIIVN	----	QYEGGLIFRLGRV	GI 1591514
68	PVLDRI	----	RVVQSLKE	----	IVINVP	789094
86	PCTDSF-IKVDM	----	RTISFDI	----	PPQEI	GI 31069
91	PCIESY-TKVVD	----	RLRTVSFS	----	VPPOE	GI 1065452
118	PCIDTTH-KVTMSITAFN	----	VVPPLQ	----	IIITDR	GI 1353669
56	PFIDRV	----	RVVVSFP	----	PPQPV	GI 79701
55	PFIDVP-VKVD	----	MRTRV	----	TDIP	GI 1591514
108	RIMDPYKAS	----	YGVDP	----	PEYAV	789094
125	RVQNA	----	TLAVANIT	----	NADSA	GI 31069
130	RI	----	SNA	----	TVSVAN	GI 1065452
157	KIR	----	PPIA	----	VCGVQD	GI 1353669
96	QV	----	TVPPQA	----	AVYEIS	GI 79701
94	RV	----	IDVEKA	----	ILEVED	GI 1591514

FIGURE 2A

148	R	-	-	E	R	E	S	L	N	A	S	I	V	D	A	I	N	O	A	A	D	C	W	G	I	R	C	L	R	Y	E	I	K	D	I	H	V	P	P	R	789094
165	S	-	-	D	R	E	E	I	A	H	N	M	Q	S	T	L	D	D	A	T	D	A	W	G	I	K	V	E	R	V	E	I	K	D	V	K	L	P	V	Q	GI 31069
170	S	-	-	D	R	E	T	L	A	S	M	Q	T	I	L	D	E	A	T	E	S	W	G	I	K	V	E	R	V	E	I	K	D	V	R	L	P	I	Q	GI 1065452	
197	S	S	Q	D	R	R	I	I	S	A	N	L	K	D	E	L	G	S	F	T	C	Q	F	G	V	E	I	T	D	V	E	I	S	D	V	K	I	-	-	GI 1353669	
136	T	-	-	S	R	D	Q	I	N	A	Q	L	R	G	V	L	D	E	A	T	G	R	W	G	L	R	V	A	R	V	E	L	R	S	I	D	P	P	S	Z79701	
134	N	-	-	K	R	E	Y	I	N	S	K	L	L	E	I	L	D	R	E	T	D	A	W	G	V	R	I	E	K	V	E	V	K	E	I	D	P	F	E	GI 1591514	
186	V	K	E	S	M	O	M	O	V	E	A	E	R	R	K	R	A	T	V	L	E	S	E	G	T	R	E	S	A	I	N	V	A	E	G	K	K	Q	A	Q	789094
203	L	Q	R	A	M	A	A	E	A	E	A	S	R	E	A	R	A	K	V	I	A	A	E	G	E	M	N	A	-	-	-	-	-	-	-	-	-	-	-	GI 31069	
208	L	Q	R	A	M	A	A	E	A	E	A	T	R	E	A	R	A	K	V	I	A	A	E	G	E	Q	K	A	-	-	-	-	-	-	-	-	-	-	GI 1065452		
234	V	K	E	G	E	N	M	G	M	S	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1353669			
174	I	Q	A	S	M	E	K	Q	M	K	A	D	R	E	K	R	A	M	I	L	T	A	E	G	T	R	E	A	A	I	K	Q	A	E	G	Q	K	L	W	Q	Z79701
172	I	K	N	A	M	A	Q	Q	M	K	A	E	R	L	K	R	A	A	I	L	E	A	E	G	E	K	P	E	-	-	-	-	-	-	-	-	-	-	GI 1591514		
226	I	L	A	S	E	A	E	K	A	E	Q	I	N	Q	A	G	E	A	S	A	V	L	A	K	A	K	A	E	A	I	-	-	-	-	-	-	-	-	789094		
231	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 31069			
236	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1065452			
260	V	I	G	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1353669			
214	I	L	A	E	G	A	K	Q	A	A	I	L	A	E	A	D	R	Q	S	R	M	L	R	A	Q	G	E	R	A	A	Y	L	Q	A	Q	Q	Q	Z79701			
259	-	R	I	L	A	A	A	L	T	O	H	N	G	D	A	A	A	S	L	T	V	A	E	Q	Y	V	S	A	F	S	K	L	A	K	D	S	N	T	I	L	789094
244	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 31069			
249	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1065452			
288	S	D	V	P	S	T	S	A	A	G	T	S	T	D	T	P	N	I	P	S	I	D	I	D	H	L	I	S	V	A	S	L	A	M	D	E	H	-	L	V	GI 1353669
254	A	K	A	I	E	K	T	F	A	A	I	K	A	G	R	P	T	P	E	M	L	A	Y	Q	Y	L	Q	T	L	P	E	M	A	R	G	D	A	N	K	V	Z79701
298	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	789094			
268	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 31069			
269	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1065452			
327	R	L	I	G	R	V	F	Q	I	N	C	K	D	I	E	P	-	I	C	I	D	L	K	H	G	S	G	S	A	Y	K	G	T	S	L	-	-	N	P	D	GI 1353669
294	W	V	P	S	D	F	N	A	L	Q	G	F	T	R	L	L	G	K	P	G	E	D	G	V	F	-	R	F	E	P	S	P	V	E	D	Q	P	K	Z79701		

FIGURE 2B

330	S L S G S S R D V Q G	- - - - -	T D A S X	D E E L D	- - - - -	R V K	- - - - -	789094
276	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
276	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	L GI 31069
364	V V F E - T S L E V F G	K I L T K E V S P V T V Y M N G N L K	V K	G S I Q D A M	G I 1065452	- - - - -	- - - - -	- - - - -
333	H A A D G D D A E V A G	W F S T D T D P S	I A R A V A - - -	T A E A I A R K P V	Z 79701	- - - - -	- - - - -	- - - - -

FIGURE 2C

Library	Lib Description	Abun	Pct	Abun
PROSTUT03	prostate tumor, 67 M, match to PROSNOT05	2	0.0703	
COLNNOT05	colon, 40 M, match to COLNCRT01	2	0.0577	
TESTNOT03	testis, 37 M	1	0.0557	
LIVRNOT02	liver, 32 F	1	0.0515	
HUVENOB01	HUVEC endothelial cell line, control	1	0.0418	
LVENNOT03	heart, left ventricle, 31 M	1	0.0336	
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0309	
PANCTUT02	pancreatic tumor, carcinoma, 45 F	1	0.0288	
KERANOT01	keratinocytes, neonatal M	1	0.0227	
CRBLNOT01	brain, cerebellum, 69 M	1	0.0194	
LUNGNOT04	lung, 2 M	1	0.0182	
PGANNT01	paraganglia, 46 M	1	0.0159	
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0150	

[illegible]

FIGURE 3